

FIG. 1A

1 AGACAGCGGAAC TAAGAAAGAGAGCCTGTGGACAGAACAAATCATGTCTGACTCCCTG
-----+-----+-----+-----+-----+-----+
MetSerAspSerLeu 60

61 GTGGTGTGCGAGGTAGACCCAGAGCTAACAGAAAAGCTGAGGAAATTCGCTTCCGAAAA
-----+-----+-----+-----+-----+-----+
ValValCysGluValAspProGluLeuThrGluLysLeuArgLysPheArgPheArgLys 120

121 GAGACAGACAATGCAGCCATCATAATGAAGGTGGACAAAGACCGCAGATGGTGGTGCTG
-----+-----+-----+-----+-----+-----+
GluThrAspAsnAlaAlaIleIleMetLysValAspLysAspArgGlnMetValValLeu 180

181 GAGGAAGAAATTCAGAACATTTCCCCAGAGGAGCTCAAAATGGAGTTGCCGGAGAGACAG
-----+-----+-----+-----+-----+-----+
GluGluGluPheGlnAsnIleSerProGluGluLeuLysMetGluLeuProGluArgGln 240

241 CCCAGGTCGTGGTTACAGCTACAAGTACGTGCATGACGATGGCCGAGTGTCCTACCCCT
-----+-----+-----+-----+-----+-----+
ProArgPheValValTyrSerTyrLysTyrValHisAspAspGlyArgValSerTyrPro 300

FIG. 1B

301 TTGTGTTTCATCTTCTCCAGCCCTGTGGGCTGCAAGCCGGAACAACAGATGATGTATGCA
 360 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
 LeuCysPheIlePheSerSerProValGlyCysLysProGluGlnGlnMetMetTyrAla
 361 GGGAGTAAAAACAGGCTGGTGCAGACAGCAGAGCTCACAAAGGTGTTTCGAAAATCCGCACC
 420 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
 GlySerLysAsnArgLeuValGlnThrAlaGluLeuThrLysValPheGluIleArgThr
 421 ACTGATGACCTCACTGAGGCCCTGGCTCCAAAGAAAGTGTCTTCTTTCGTTGATCTCTG
 480 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
 ThrAspAspLeuThrGluAlaTrpLeuGlnGluLysLeuSerPhePheArg
 541 GGCTGGGACTGAATTCCTGATGTCTGAGTCCTCAAGGTGACTGGGGACTTGGAAACCCCT
 600 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
 AGGACCTGAACAACCAAGACTTTAAATAAAATTTTAAATGCAAAAAAATAAAAAA
 660 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +

FIG. 2

Query: 46 MSDSLVCVDPPELTKLRKFRFRKETDNAAIIMKVDKDRQMVL EEEFQNISPEELKME 225
MS+SLVVC+V +L EKLKFRFRKET+NAAIIMK+DKD+++VVL+EE + ISP+ELK E
Sbjct: 1 MSELVVCDAEDLVEKLRKFRFRKETNNAAIIMKIDKRLVVLDEELEGISPDELKDE 60

Query: 226 LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 405
LPERQPRF+VYSYKY HDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKN+LVQTAELTKV
Sbjct: 61 LPERQPRFIVYSYKYQHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNKL VQTAELTKV 120

Query: 406 FEIRTTDDLTEAWLQELKLSFF 468
FEIR T+DLTE WL+EKL FF
Sbjct: 121 FEIRNTEDLTEEWLREKL GFF 141

10004832.120701

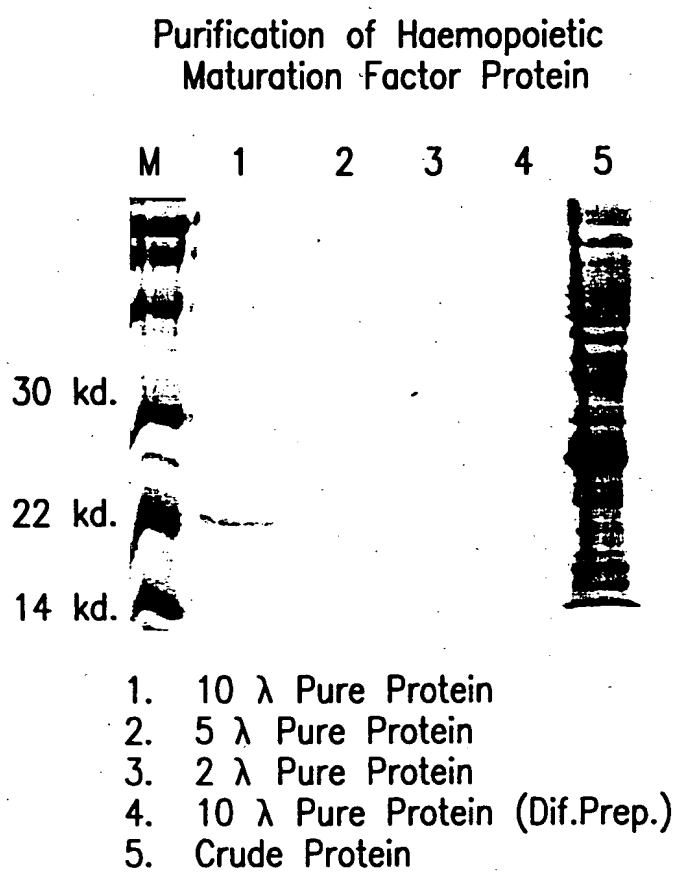


FIG.3

ANALYSIS OF THE HAEMOPOIETIC MATURATION FACTOR EXPRESSION MEDIA USING
REVERSED-PHASE HPLC

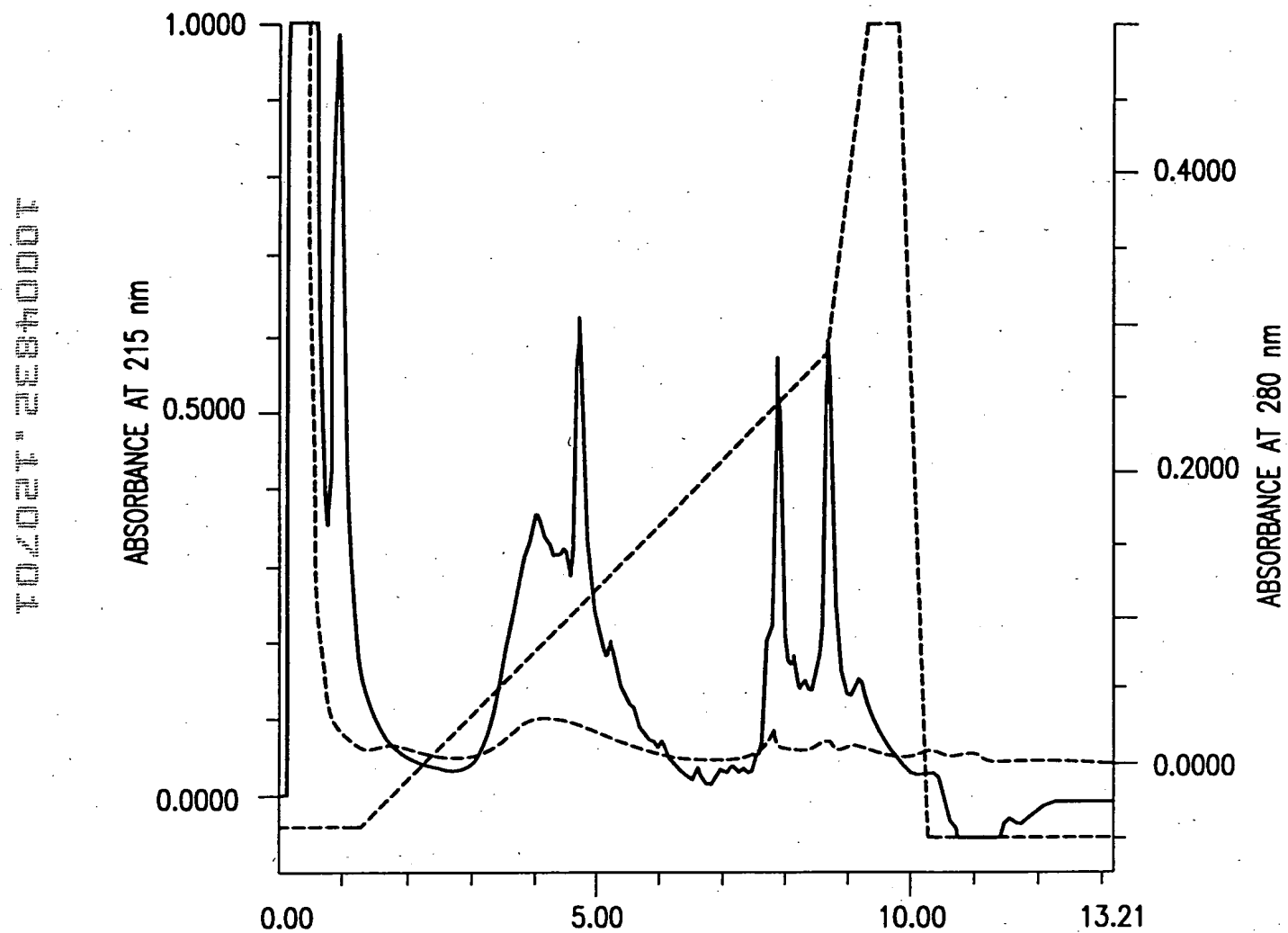


FIG.4A

ANALYSIS OF THE HAEMOPOIETIC MATURATION FACTOR EXPRESSION MEDIA BY
REVERSED-PHASE HPLC AFTER PURIFICATION.

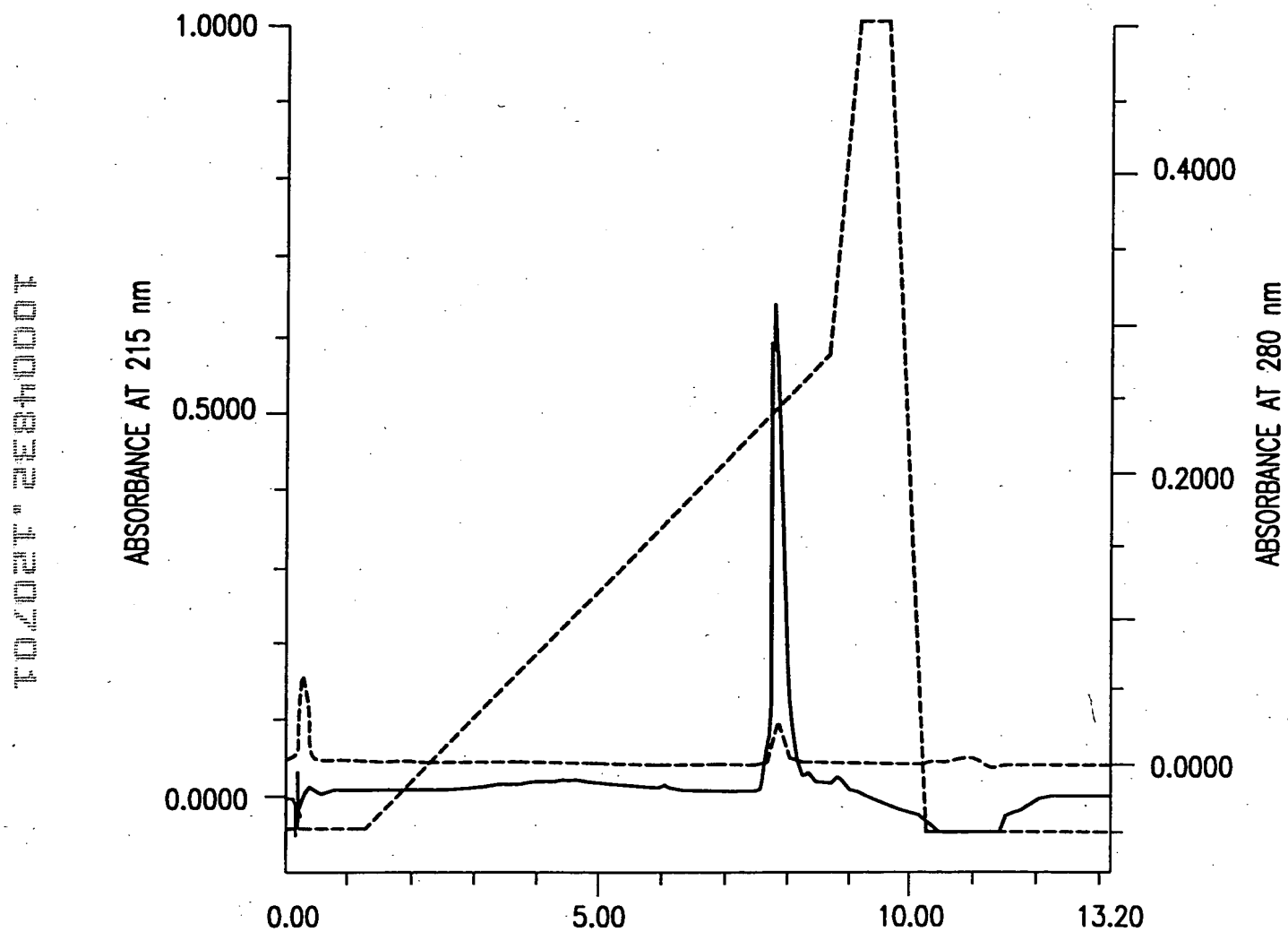


FIG.4B

QUANTIFICATION OF HUMAN MONOCYTE NORTHERN BLOT
PROBED WITH HAEMOPOIETIC MATURATION FACTOR

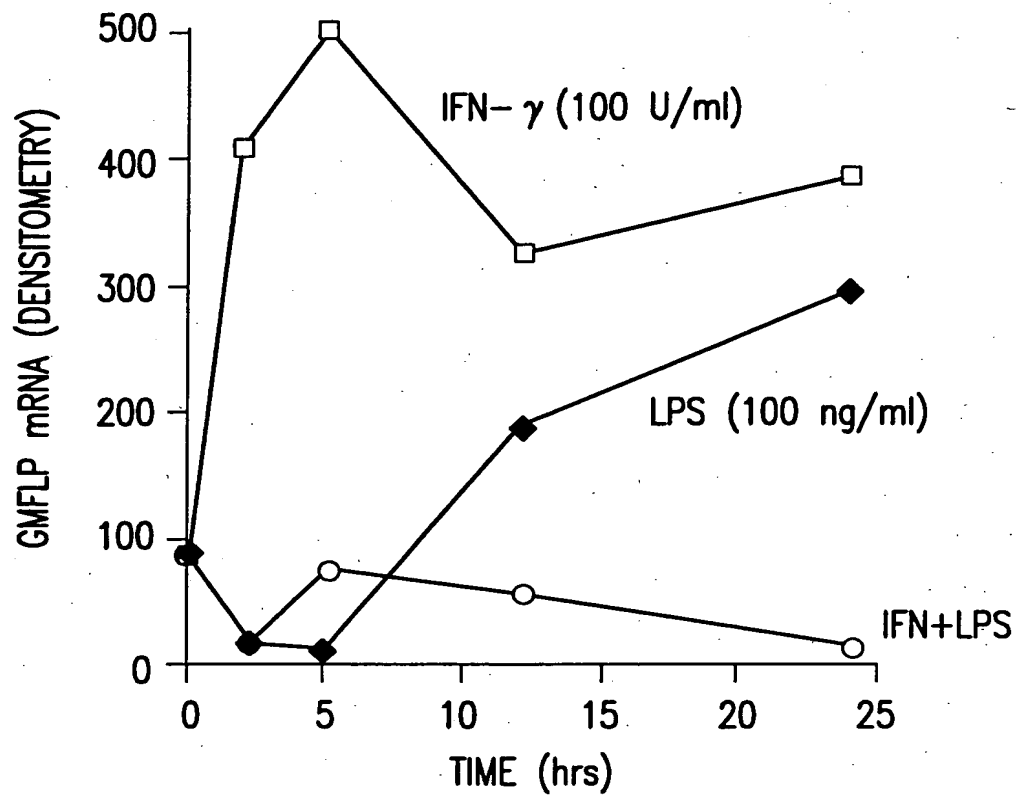


FIG.5

FOOT-2534000T

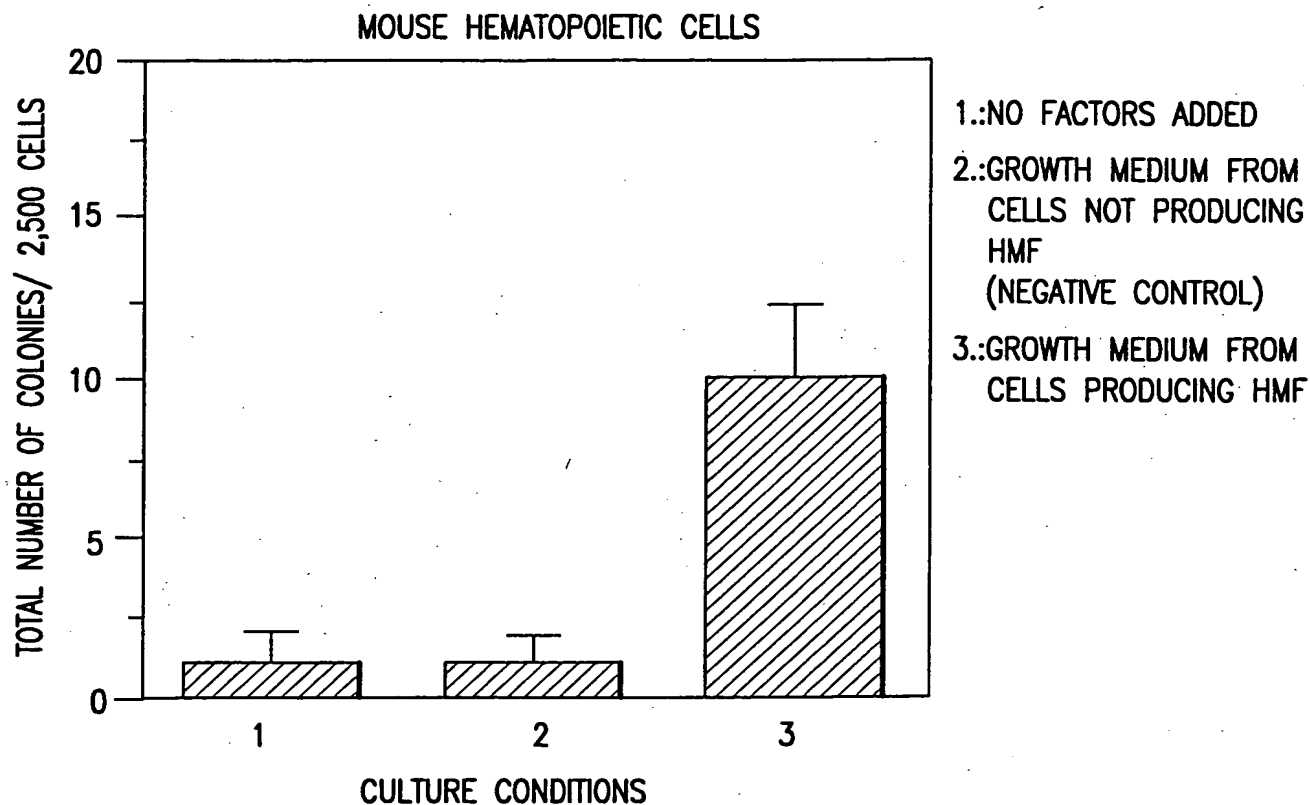


FIG.6A

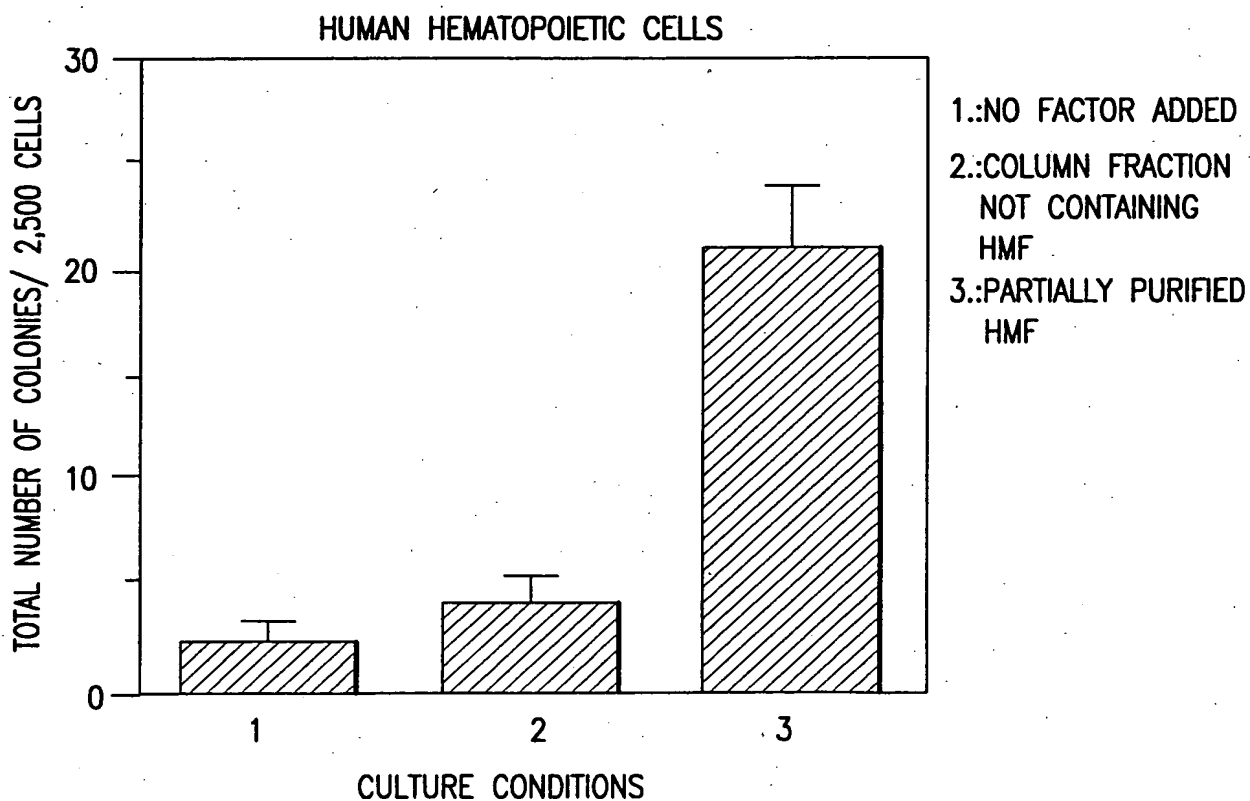


FIG.6B